

Amendments to the Drawings:

Amended drawing sheets of Figures 12A - 12F are attached as replacement sheets.



Table 1
Summary of the effects of Peptides on Ab42 fibril
Analyzed at Ab42:Peptide wt/wt ratio of 1:2

SEQ ID NO:				% Loss of 218 CD ellipticity
1	RKRLQVQLSIRT #	AG73 or A1	12aa	-21.6 (gain)
3	RQVFQVAYIIKA ###	A13	13aa	37.5
8	YLSKGRLVFALG	HA3G76	12aa	58.5 *
11	TLFLAHGRLVFM ##	A4G82	12aa	85.6 ***
15	AGQWHRVSVRWG	A5G81	12aa	91.6 *****
18	DGRWHRVAVIMG	A5G101	12aa	89.0 *****
4	HQTWTRNLQVTL	HA3G47	12aa	-20.2 (gain)
5	ISNVFVQRLSLS	HA3G58	12aa	3.85
7	RGLVFHTGTKNSF	HA3G74	13aa	34.4
10	GNSTISIRAPVY	HA3G83	12aa	30.5
16	VRWGMQQLVV	A5G82	12aa	27.6
19	APVNVTVASVQIQ	A5G109	12aa	14.9
34	TRISLQVQLRKR #	rAG73 or A1	12aa	43.3
35	AKIIIVAVQFVQR ###	rA13	13aa	7.0
36	GLAFVLRGKSLY	rHA3G76	12aa	76.0 ***
37	MFVLRGHALFLT ##	rA4G82	12aa	48.1
38	GWRVSVRHWQGA	rA5G81	12aa	58.6 **
39	GMIVAVRHWRGD	rA5G101	12aa	48.8

PTI-	SEQ ID NO:	Structure	Formula	MW
DP-001 D-AG73 or D-A1 A1-chain 2719-2730	1	Arg-Lys-Arg-Leu-Gln-Val-Gln-Leu-Ser-Ile-Arg-Thr 	$C_{64}H_{120}N_{24}O_{17}$	1497.82
DP-002 D-A13 A1-chain 97-109	3	Arg-Gln-Val-Phe-Gln-Val-Ala-Tyr-Ile-Ile-Ile-Lys-Ala 	$C_{74}H_{121}N_{19}O_{17}$	1548.90
DP-003 D-HA3G76 A3-chain 1418-1429	8	Tyr-Leu-Ser-Lys-Gly-Arg-Leu-Val-Phe-Ala-Leu-Gly 	$C_{63}H_{102}N_{16}O_{15}$	1323.61
DP-004 D-A4G82 A4-chain 1513-1524	11	Thr-Leu-Phe-Leu-Ala-His-Gly-Arg-Leu-Val-Phe-Met 	$C_{67}H_{105}N_{17}O_{14}S$	1404.75
DP-005 D-A5G81 A5-chain 3337-3348	15	Ala-Gly-Gln-Trp-His-Arg-Val-Ser-Val-Arg-Trp-Gly 	$C_{65}H_{95}N_{23}O_{15}$	1438.62
DP-006 D-A5G101 A5-chain 3516-3527	18	Asp-Gly-Arg-Trp-His-Arg-Val-Ala-Val-Ile-Met-Gly 	$C_{61}H_{97}N_{21}O_{15}S$	1396.65
DP-007 D-HA3G47 A3-chain 1189-2000	4	His-Gln-Thr-Trp-Thr-Arg-Asn-Leu-Gln-Val-Thr-Leu 	$C_{66}H_{105}N_{21}O_{19}$	1496.70
DP-008 D-HA3G58 A3-chain 1276-1287	5	Ile-Ser-Asn-Val-Phe-Val-Gln-Arg-Leu-Ser-Leu-Ser 	$C_{61}H_{103}N_{17}O_{18}$	1362.60

Figure 12A

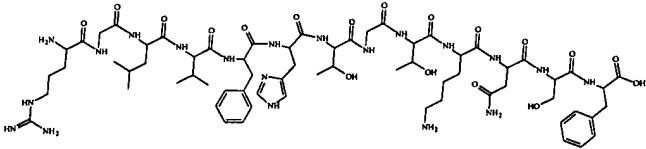
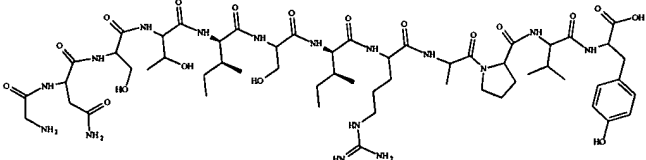
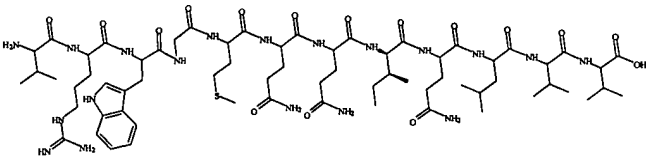
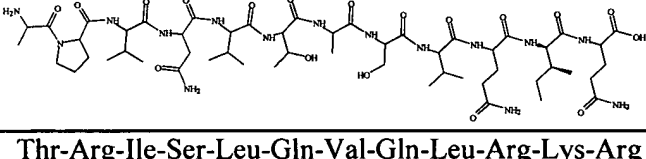
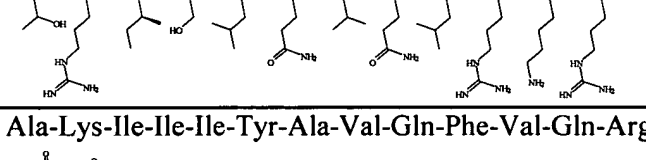
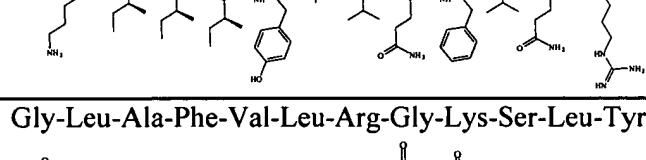
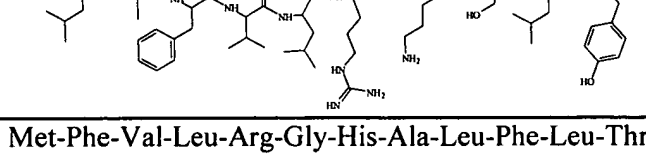
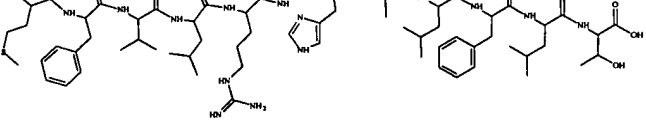
PTI-	SEQ ID NO:	Structure	Formula	MW
DP-009 D-HA3G74 A3-chain 1402-1414	7	Arg-Gly-Leu-Val-Phe-His-Thr-Gly-Thr-Lys-Asn-Ser-Phe 	$C_{66}H_{102}N_{20}O_{18}$	1463.67
DP-010 D-HA3G83 A3-chain 1477-1487	10	Gly-Asn-Ser-Thr-Ile-Ser-Ile-Arg-Ala-Pro-Val-Tyr 	$C_{56}H_{92}N_{16}O_{18}$	1277.45
DP-011 D-A5G82 A5-chain 3345-3356	16	Val-Arg-Trp-Gly-Met-Gln-Gln-Ile-Gln-Leu-Val-Val 	$C_{66}H_{109}N_{19}O_{16}S$	1456.78
DP-012 D-A5G109 A3-chain 1444-1455	19	Ala-Pro-Val-Asn-Val-Thr-Ala-Ser-Val-Gln-Ile-Gln 	$C_{53}H_{91}N_{15}O_{18}$	1226.40
DP-013 D-rAG73 or D-rA1 A1-chain r2719-2730 or 2730-2719	34	Thr-Arg-Ile-Ser-Leu-Gln-Val-Gln-Leu-Arg-Lys-Arg 	$C_{64}H_{120}N_{24}O_{17}$	1497.82
DP-014 D-rA13 A1-chain r92-109 or 109-92	35	Ala-Lys-Ile-Ile-Ile-Tyr-Ala-Val-Gln-Phe-Val-Gln-Arg 	$C_{74}H_{121}N_{19}O_{17}$	1547.92
DP-015 D-rHA3G76 A3-chain r1418-1429 or 1429-1418	36	Gly-Leu-Ala-Phe-Val-Leu-Arg-Gly-Lys-Ser-Leu-Tyr 	$C_{63}H_{102}N_{16}O_{15}$	1323.61
DP-016 D-rA4G82 A4-chain r1513-1524 or 1524-1513	37	Met-Phe-Val-Leu-Arg-Gly-His-Ala-Leu-Phe-Leu-Thr 	$C_{67}H_{105}N_{17}O_{14}S$	1404.75

Figure 12B

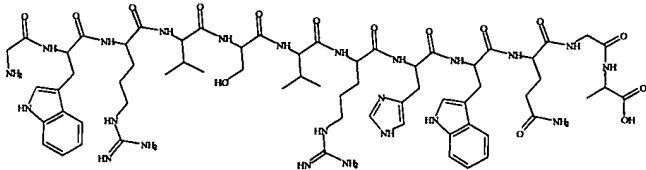
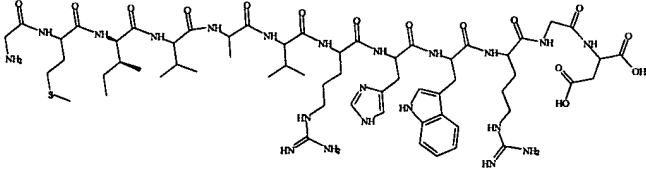
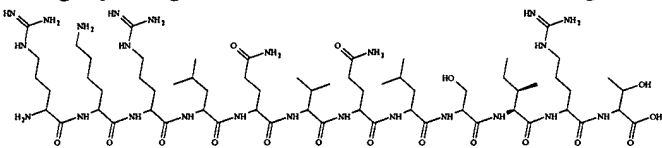
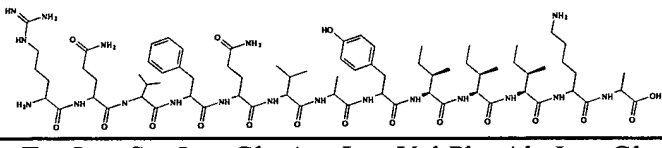
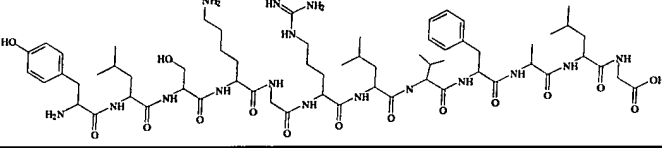
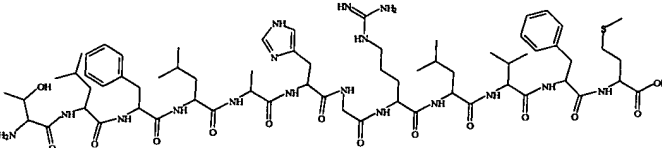
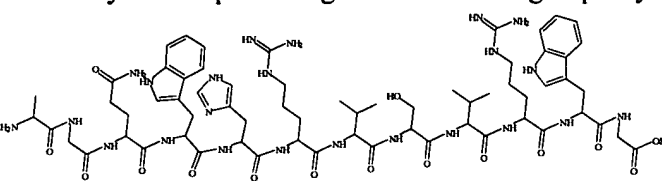
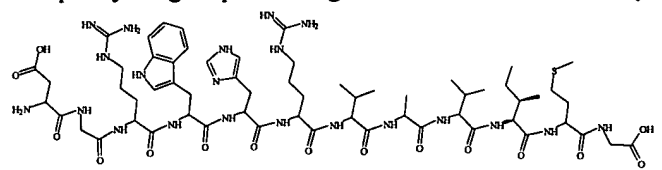
PTI-	SEQ ID NO:	Structure	Formula	MW
DP-017 D-rA5G81 A5-chain r3337-3348 or 3348-3337	38	Gly-Trp-Arg-Val-Ser-Val-Arg-His-Trp-Gln-Gly-Ala 	$C_{65}H_{95}N_{23}O_{15}$	1438.62
DP-018 D-rA5G101 A5-chain r3516-3527 or 3527-3516	39	Gly-Met-Ile-Val-Ala-Val-Arg-His-Trp-Arg-Gly-Asp 	$C_{61}H_{97}N_{21}O_{15}S$	1396.65
LP-019 AG73 or A1 A1-chain 2719-2730	1	Arg-Lys-Arg-Lue-Gln-Val-Gln-Leu-Ser-Ile-Arg-Thr 	$C_{64}H_{120}N_{24}O_{17}$	1497.82
LP-020 A13 A1-chain 92-109	3	Arg-Gln-Val-Phe-Gln-Val-Ala-Tyr-Ile-Ile-Ile-Lys-Ala 	$C_{74}H_{121}N_{19}O_{17}$	1548.90
LP-021 HA3G76 A3-chain 1418-1429	8	Tyr-Leu-Ser-Lys-Gly-Arg-Leu-Val-Phe-Ala-Leu-Gly 	$C_{63}H_{102}N_{16}O_{15}$	1323.61
LP-022 A4G82 A4-chain 1513-1524	40	Thr-Leu-Phe-Phe-Met-Arg-Leu-Val-His-Ala-Leu-Gly 	$C_{67}H_{105}N_{17}O_{14}S$	1404.75
LP-023 A5G81 A5-chain 3337-3348	15	Ala-Gly-Gln-Trp-His-Arg-Val-Ser-Val-Arg-Trp-Gly 	$C_{65}H_{95}N_{23}O_{15}$	1438.62
LP-024 A5G101 A5-chain 3516-3527	18	Asp-Gly-Arg-Trp-His-Arg-Val-Ala-Val-Ile-Met-Gly 	$C_{61}H_{97}N_{21}O_{15}S$	1396.65

Figure 12C

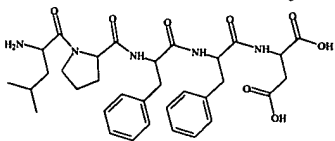
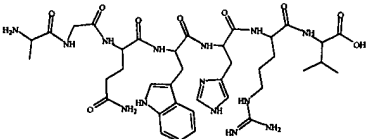
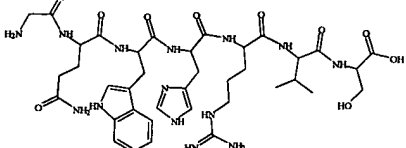
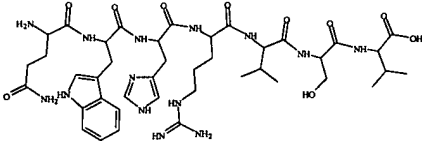
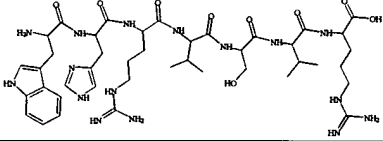
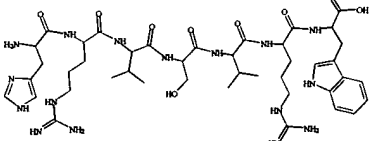
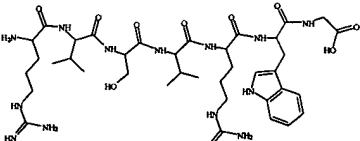
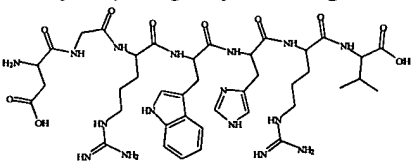
PTI-	SEQ ID NO:	Structure	Formula	MW
LP-025 β-sheet breaker or iAβ5	41	<p>Leu-Pro-Phe-Phe-Asp</p> 	$C_{33}H_{43}N_5O_8$	637.74
DP-026 Trc'n 5;1-7	42	<p>Ala-Gly-Gln-Trp-His-Arg-Val</p> 	$C_{38}H_{56}N_{14}O_9$	852.95
DP-027 Trc'n 5;2-8	43	<p>Gly-Gln-Trp-His-Arg-Val-Ser</p> 	$C_{38}H_{56}N_{14}O_{10}$	868.95
DP-028 Trc'n 5;3-9	44	<p>Gln-Trp-His-Arg-Val-Ser-Val</p> 	$C_{41}H_{62}N_{14}O_{10}$	911.04
DP-029 Trc'n 5;4-10	45	<p>Trp-His-Arg-Val-Ser-Val-Arg</p> 	$C_{42}H_{66}N_{16}O_9$	939.09
DP-030 Trc'n 5;5-11	46	<p>His-Arg-Val-Ser-Val-Arg-Trp</p> 	$C_{42}H_{66}N_{16}O_9$	939.09
DP-031 Trc'n 5;6-12	47	<p>Arg-Val-Ser-Val-Arg-Trp-Gly</p> 	$C_{38}H_{62}N_{14}O_9$	859.00
DP-032 Trc'n 6;1-7	48	<p>Asp-Gly-Arg-Trp-His-Arg-Val</p> 	$C_{40}H_{60}N_{16}O_{10}$	925.02

Figure 12D

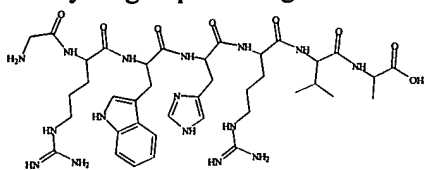
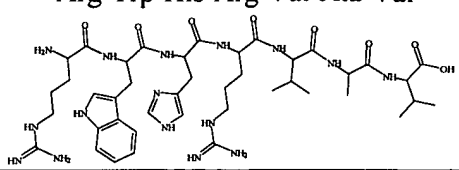
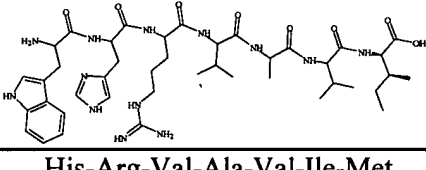
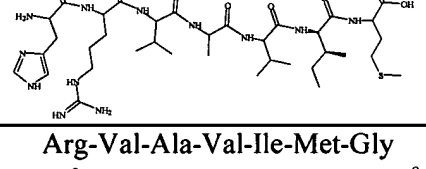
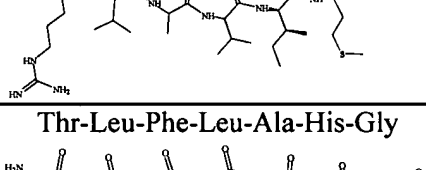
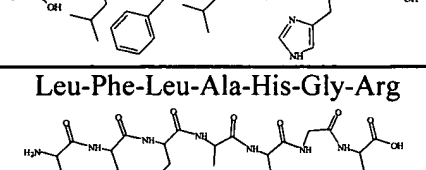
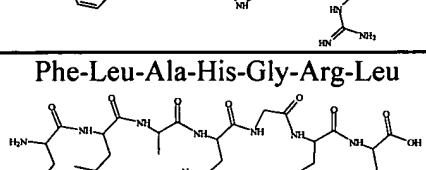
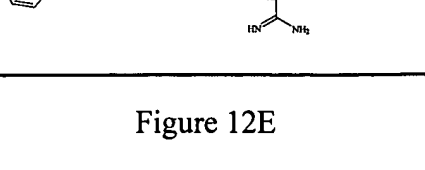
PTI-	SEQ ID NO:	Structure	Formula	MW
DP-033 Trc'n 6;2-8	49	<p>Gly-Arg-Trp-His-Arg-Val-Ala</p> 	$C_{39}H_{60}N_{16}O_8$	881.01
DP-034 Trc'n 6;3-9	50	<p>Arg-Trp-His-Arg-Val-Ala-Val</p> 	$C_{42}H_{66}N_{16}O_8$	923.09
DP-035 Trc'n 6;4-10	51	<p>Trp-His-Arg-Val-Ala-Val-Ile</p> 	$C_{42}H_{65}N_{13}O_8$	880.07
DP-036 Trc'n 6;5-11	52	<p>His-Arg-Val-Ala-Val-Ile-Met</p> 	$C_{36}H_{64}N_{12}O_8S$	825.05
DP-037 Trc'n 6;6-12	53	<p>Arg-Val-Ala-Val-Ile-Met-Gly</p> 	$C_{32}H_{60}N_{10}O_8S$	744.96
DP-038 Trc'n 4;1-7	54	<p>Thr-Leu-Phe-Leu-Ala-His-Gly</p> 	$C_{36}H_{55}N_9O_9$	757.89
DP-039 Trc'n 4;2-8	55	<p>Leu-Phe-Leu-Ala-His-Gly-Arg</p> 	$C_{38}H_{60}N_{12}O_8$	812.97
DP-040 Trc'n 4;3-9	56	<p>Phe-Leu-Ala-His-Gly-Arg-Leu</p> 	$C_{38}H_{60}N_{12}O_8$	812.98

Figure 12E

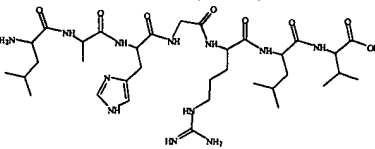
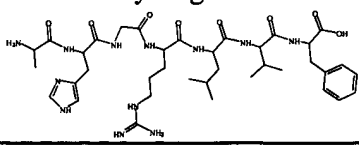
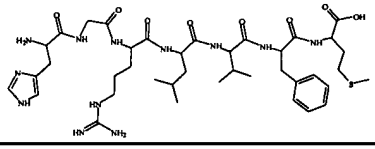
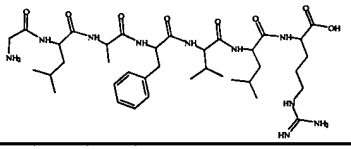
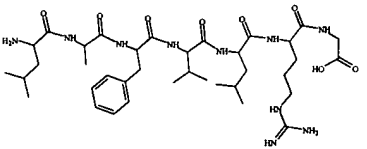
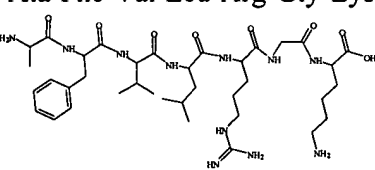
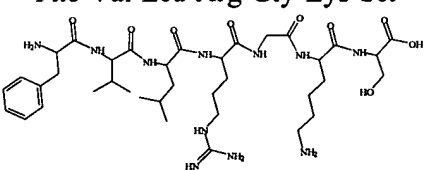
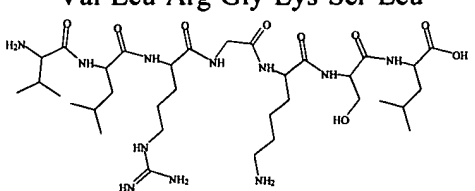
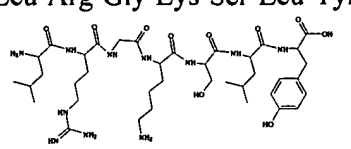
PTI-	SEQ ID NO:	Structure	Formula	MW
DP-041 Trc'n 4;4-10	57	<p>Leu-Ala-His-Gly-Arg-Leu-Val</p> 	$C_{34}H_{60}N_{12}O_8$	764.93
DP-042 Trc'n 4;5-11	58	<p>Ala-His-Gly-Arg-Leu-Val-Phe</p> 	$C_{37}H_{58}N_{12}O_8$	798.95
DP-043 Trc'n 4;6-12	59	<p>His-Gly-Arg-Leu-Val-Phe-Met</p> 	$C_{39}H_{62}N_{12}O_8S$	859.07
DP-044 Trc'n 15;1-7	60	<p>Gly-Leu-Ala-Phe-Val-Leu-Arg</p> 	$C_{37}H_{62}N_{10}O_8$	774.97
DP-045 Trc'n 15;2-8	61	<p>Leu-Ala-Phe-Val-Leu-Arg-Gly</p> 	$C_{37}H_{62}N_{10}O_8$	774.97
DP-046 Trc'n 15;3-9	62	<p>Ala-Phe-Val-Leu-Arg-Gly-Lys</p> 	$C_{37}H_{63}N_{11}O_8$	789.98
DP-047 Trc'n 15;4-10	63	<p>Phe-Val-Leu-Arg-Gly-Lys-Ser</p> 	$C_{37}H_{63}N_{11}O_9$	805.98
DP-048 Trc'n 15;5-11	64	<p>Val-Leu-Arg-Gly-Lys-Ser-Leu</p> 	$C_{34}H_{65}N_{11}O_9$	771.96
DP-049 Trc'n 15;6-2	6	<p>Leu-Arg-Gly-Lys-Ser-Leu-Tyr</p> 	$C_{38}H_{65}N_{11}O_{10}$	836.01

Figure 12F